

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2005, 12:53:59 ; Search time 6727 Seconds

(without alignments)  
8650.916 Million cell updates/sec

Title: US-09-836-544B-28

Perfect score: 1201

Sequence: 1 ggggtgcaaaggagacag.....aaataaagtgacagatgacc 1201

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Genbank:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sb:  
12: gb\_by:  
13: gb\_un:  
14: gb\_vl:  
14:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1201	100.0	BD015201	BD015201 LOCUS DEFINITION
2	1201	100.0	AR380482	TDLSA cell surface antigen and CD27 cell surface antigen, and utilization thereof.
3	1201	100.0	AK697951	ACCESSION VERSION
4	1201	100.0	AX818155	JP 2001157592-A/19;
5	1201	100.0	HUMCD27A	SOURCE
6	1201	100.0	BC012160	ORGANISM
7	1199.4	99.9	C721686	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
8	1199.4	99.9	CQ869620	1 (bases 1 to 1201)
9	524	43.6	AK778265	REFERENCE
10	451.8	37.6	AK778267A	AUTHORS
11	444.4	37.0	AC00604	Seed,B.; Aruffo,A. and Amiot,M.
12	442.8	36.9	AY04961	TITLE
13	442.8	36.9	CQ869619	TDLSA cell surface antigen and CD27 cell surface antigen, and utilization thereof.
14	441.2	36.7	AC005840	PATENT
15	408.8	34.0	CQ869620	JP 2000305557
16	369.4	30.8	AK778265	PI
17	369.4	30.8	AK778267A	BRIAN SEED,ALBANIANO ARUFFO,MARTIN AMIOT
18	318.2	26.5	AC00604	PC
c 19	249.8	20.8	AK056500	C12N15/09,C07K14/725,G01N33/53,C12N15/00

#### ALIGNMENTS

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c 24	235.8	19.6	483	6	CQ174565 Sequence
c 25	235.8	19.6	483	6	CQ220018 Sequence
c 26	235.8	19.6	483	6	CQ258428 Sequence
c 27	235.8	19.6	483	6	CQ295823 Sequence
c 28	235.8	19.6	483	6	CQ332386 Sequence
c 29	234.4	19.5	455	6	CQ079331 Sequence
c 30	234.4	19.5	455	6	CQ111004 Sequence
c 31	234.4	19.5	455	6	CQ149761 Sequence
c 32	234.4	19.5	455	6	CQ184470 Sequence
c 33	234.4	19.5	455	6	CQ233050 Sequence
c 34	234.4	19.5	455	6	CQ271024 Sequence
c 35	234.4	19.5	455	6	CQ308362 Sequence
c 36	234.4	19.5	455	6	CQ345153 Sequence
c 37	225.4	18.8	1028	9	HUMCD27A Human anti-g
c 38	135	11.2	5429	6	AX251343 Sequence
c 39	135	11.2	5429	6	AK346746 Sequence
c 40	123.6	10.3	4728	6	CQ869616 Sequence
c 41	123.6	10.3	20765	2	AC140324 Mus muscu
c 42	114.2	9.5	5429	6	AX251344 Sequence
c 43	114.2	9.5	5429	6	AC346747 Rattus no
c 44	112.2	9.3	21052	2	AC128082 Rattus no
c 45	112.2	9.3	232984	2	AC11597 Rattus no

#### FEATURES

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13	442.8	36.9	26815	6	36.9%	1201	6	1201
14	441.2	36.7	140026	9	36.7%	1201	6	1201
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18				
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Query	Match	Score	Length	DB
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881. .1204

**ORIGIN** 3' UTR

Query Match 100.0%; Score 1201; DB 6; Length 1204;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-281; Mismatches 0; Indels 0; Gaps 0;  
 Matches 1201; Conservative 0; Pairs 0; Gaps 0;

QY	1	GGGTCAMAGAGAGACAGCAGGCCAGCTTGAGGTTCAACTCCAGGGCCAGAT
Db	1	GGGTGCAAGAAGAGACAGCAGGCCAGCTTGAGGTTCAACTCCAGGGCCAGAT
QY	61	CAGCACTTGGCACAGAAAGAGGCCAGCTTGAGGTTCAACTCCAGGGCCAGAT
Db	61	CAGCACTTGGCACAGAAAGAGGCCAGCTTGAGGTTCAACTCCAGGGCCAGAT
QY	121	GTGGGTGCGTTCTGGGACCCCTGTGGAGGCTTAAGCTTCAAGGAGAGCTG
Db	121	GTGGGTGCGTTCTGGGACCCCTGTGGAGGCTTAAGCTTCAAGGAGAGCTG
QY	181	CCCAGAGGAGCACTACTGGCTTCTGAGGGAGAGCTGAGGAGAGCTG
Db	181	CCCAGAGGAGCACTACTGGCTTCTGAGGGAGAGCTGAGGAGAGCTG
QY	241	ATTCTCTGCTGAGGACTGTGCAACGAGCATGAGAACGCTGCTAGTGATCTTGTAC
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Db	301	GGGGGTCTCTCTCTCTGACACCACACACACACACACACACACACACACACAC
QY	361	TAACTCTGGCTTCCTCGTCTGCAACTGCACACACACACACACACACACACAC
Db	361	TAACTCTGGCTTCCTCGTCTGCAACTGCACACACACACACACACACACACAC
QY	421	CAATGCTCTGAGGCTGAGGCAACAGGAGTCACCGAGTCACCGAGTCACCG
Db	421	CAATGCTCTGAGGCTGAGGCAACAGGAGTCACCGAGTCACCGAGTCACCG
QY	481	CTCTGACCGCTGGCTCTGAGGCCACACCCCTGAGCCACCCCTAGCCACCCACTAC
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QY	541	TGTCACTGAGATGCTGGAGGCCAGGACAGCTGGCACTCTGGTACTCTGAGTC
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QY	661	CGATTTTATTCGCACTCTGAGCTCTCTCTGGATGTTCTTCTTCTTCTTCTTCT
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/note="unnamed protein product"

RESULTS

RESULT 3

AX697951 AX697951 1204 bp DNA linear PAT 02-APR-2003

Locus AX697951 Sequence 1 from Patent WO03009862.

Definition AX697951.1 GI:29499010

Accession AX697951.1 Version

KeyWords

Source Homo sapiens (human)

Organism Homo sapiens

Definition Sequence 1 from Patent WO03009862.

Version AX697951.1 GI:29499010

KeyWords

Source Homo sapiens (human)

Organism Homo sapiens

Definition Sequence 1 from Patent WO03009862.

Version AX697951.1 GI:29499010

KeyWords

Reference 1. Lucas, J., Dialynas, D. and Briggs, K.

Title Agonists and antagonists of modumet for use in the treatment of metabolic disorders

Journal Patent: WO 03009862-A 1 06-FEB-2003;

GenSet SA (FR) Location/Qualifier

Features

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1. .100  
101. .893  
5'UTR  
CDS



SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
AUTHORS	Camerini-D., Walz,G., Loenen,W.A., Borst,J. and Seed,B.
TITLE	The T cell activation antigen CD27 is a member of the nerve growth factor/tumor necrosis factor receptor gene family
JOURNAL	J. Immunol. 147 (9), 3165-3169 (1991)
MEDLINE	92131349
PUBMED	1655907
COMMENT	Original source text: Homo sapiens cDNA to mRNA.
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ORIGIN	
Query Match	100.0% Score 1201; DB 9; Length 1204;
Best Local Similarity	100.0%; Pred. No. 3.2e-281;
Matches	1201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CGGGTCAAGAAGAGACAGACAGGGCCACGCTTGAGGTGACTCCAGGGCCACAT 60
Db	1 GGGGTCAAGAAGAGACAGACAGGGCCACGCTTGAGGTGACTCCAGGGCCACAT 60
Qy	61 CAGCAACTGGCACAGAACAGAGAGACAGAGCGCCACGCTTGAGGTGACTCCCTG 120
Db	61 CAGCAACTGGCACAGAACAGAGAGACAGAGCGCCACGCTTGAGGTGACTCCCTG 120
Qy	121 GGGGNGTGCCTCTGGGACACTGGAGGGCTCTGAGTCTACCTCCAGGCCAACAGCTG 180
Db	121 GGGGNGTGCCTCTGGGACACTGGAGGGCTCTGAGTCTACCTCCAGGCCAACAGCTG 180
Qy	181 CCCAGAGAGGACTACTGGGTCAGGAACAGCTGTCGCCAGATGTTGAGCCAGGAC 240
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Qy	241 ATTCTCTGTGAGGAGCTGTGACCAGCATAGAAAGGGCTGCTAGTGTATCCTGCAATTAC 300
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Qy	301 GGGGNGTCCCTCTCTGGGACACCGACCGCCACACTGGAGCTGAGTGTGATCTTGTGATCC 360
Db	301 GGGGNGTCCCTCTCTGGGACACCGACCGCCACACTGGAGCTGAGTGTGATCTTGTGATCC 360
Qy	361 TRACTCTGTGCTCTGGGACACCATCACTGGGCTGAGTGTGATCTTGTGATCC 420
Db	361 TRACTCTGTGCTCTGGGACACCATCACTGGGCTGAGTGTGATCTTGTGATCC 420
Qy	421 CAGTGGTGGGAGTGCAAGGGACAGAGGTGTCAGCCAGTGTGATCTTGTGATCC 480
Db	421 CAGTGGTGGGAGTGCAAGGGACAGAGGTGTCAGCCAGTGTGATCTTGTGATCC 480
Qy	481 GCTGACCGCTCTGGCTGAGGCCACCTCTGAGCCACACCTCTTACCTTA 540
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Qy	541 TGTCACTGAGATGCTGGGAGGACAGCTGGCACATGAGACTCTGGTACTCTAG 600
RESULT 6	
LOCUS	BC012160
DEFINITION	Homo sapiens tumor necrosis factor receptor superfamily, member 7, mRNA (cDNA clone MGC:20393 IMAGE:4575359), complete cds.
ACCESSION	BC012160
VERSION	BC012160.1
KEYWORDS	GI:15082490
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
AUTHORS	1 (bases 1 to 123)
	Strussberg,R.I., Feingold,E.A., Grouse,L.H., Dergé,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schulier,G.D., Altschul,S.F., Zeeberg,B., Butow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J.J., Hsieh,F., Diatchenko,L., Matsunaga,A., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S., Loquelandio,N.A., Peters,G.J., Abramson,R.D., Mulahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,A.M., Garcia,L.J., Hulyk,S.W., Villalon,D.K., Muzyk,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, N., Madan, A., Young, A.C.W., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalius, D.R., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
1247932  
2 (bases 1 to 1323)

Strausberg, R.  
Direct Submission  
Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [crabps@mail.nih.gov](mailto:crabps@mail.nih.gov)

Tissue Procurement: Louis Staudt  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgc.bc.ca](mailto:info@bcgc.bc.ca)

Steve Jones, Steven Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Feathersome, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Jim MacDonald, Anna Mason, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smilios, Jeff Stott, Miranda Tsai, George Yang, Jacqueline Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: <http://image.liln.gov>  
Series: TRAL plate: 29 Row: h Column: 11  
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers

1. .1323
 

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2. .1323
 

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3. .1323
 

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RESULTS

Db	301 GAGAGTGAGGACCTGGCAGCAACTGAGTCCTCCATCTCTTCAGGCCCTTCCGT	Db	386 CCTCTCTCCAGACTACACACCGGCCACTGCGGAGCTGCAAGCATGTAACCTG
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Db	361 GTACACGTGACAGTGCTTCAGTGACTGGAGGAGGAGCAATAATGATGAGGT	Db	446 GTTTCTTATTCGGCAACTGCACTGCACTGCAATGTCAGTGCACTGCACTGCAAGACT
Qy	1069 GGAGAGTGCGAAGCAGGAGGCCAGCTGCGCCCTSGGCTSGGCTCAGAGGGCGGGGCT	Qy	429 GGGAGTGAGGACAGAGTGACTGGCAGGAGGAGCAATAATGATGAGGT
Db	421 GGAGAGTGCGAAGCAGGAGGCCAGCTGCGCCCTGCGCTGCGAGGGGGCT	Db	506 GGGAGTGAGGACAGAGTGACTGGCAGGAGGAGCAATAATGATGAGGT
Qy	1129 GGTGTAACAACTTGCTCGAAGAACCCACATGCTCA 1172	Qy	489 CTGGCTCTCAGGCCACACCTTGAGCCACACCCTGAGCCACCCACTTACCTTGCTG
Db	481 GGTGTAACAACTTGCTCGAAGAACCCACATGCTCA 524	Qy	548 AGATGCTGAGGCCAGAGTGCGACATCGAGCTCTGCTGACTTCAGGCGACTG
<b>RESULT 10</b>			
<b>LOCUS</b>	<b>MUSCD27A</b>	<b>DEFINITION</b>	1585 bp mRNA.
<b>ACCESSION</b>	Mus musculus CD27 antigen (Cd27)	<b>VERSION</b>	linear ROD 25-SEP-1993
<b>KEYWORDS</b>	Cd27 antigen.		
<b>ORGANISM</b>	Mus musculus (house mouse)		
<b>REFERENCE</b>	Makrilia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 1585)		
<b>AUTHORS</b>	Gravestein,L.A., Blom,B., Nolten,I.A., de Vries,B., van der Horst,G., Osendarp,F., Borst,J. and Loenen,W.A.		
<b>TITLE</b>	Cloning and expression of murine CD27: comparison with 4-IBB, another lymphocyte-specific member of the nerve growth factor receptor family. Eur. J. Immunol. 23 (4), 943-950 (1993)		
<b>JOURNAL</b>	9320296		
<b>PUBLISHED</b>	834562		
<b>COMMENT</b>	Original source text: Mus musculus (strain B6(CBA)F1) library: oligo dt in lambda ZAP) female Juvenile, 6-8 weeks thymus cDNA to mRNA.		
<b>FEATURES</b>	<b>source</b>		
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<b>ORIGIN</b>			
Query Match	37.6%; Score 451.8; DB 10; Length 1585;		
Best Local Similarity	73.2%; Pred. No. 5.2e-99;		
Matches	633; Conservative 0; Mismatches 202; Indels 30; Gaps 3;		
REFERENCE	1 (bases 1 to 172571)		
AUTHORS	Muzny,D.M., Adams,B., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayle,M., Banks,T., Barberia,J., Benton,J., Bimonte,K., Blankenburg,K., Bonin,D., Bouck,J., Bowie,S., Briava,M., Brown,E., Brown,M., Bryant,N.P., Buhan,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavaos,S.R., Chacko,J.J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davis,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Den,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Barnhart,C., Edgar,D., Edwards,C.C., Elhai,C., Emerling,S., Escott,M., Failes,T., Ferrando,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,J., Hart,M., Havlik,P., Hawes,A., Hernandez,J., Hernandez,O., Hodges,A., Hogenesch,B.,		
<b>RESULT 11</b>			
<b>Db</b>	AC006064	<b>LOCUS</b>	172571 bp DNA
<b>DEFINITION</b>	PRI 01-FEB-2003		
<b>ACCESSION</b>	AC006064	<b>PAC Library</b>	complete sequence.
<b>VERSION</b>	AC006064.10	<b>KEYWORDS</b>	HTG.
<b>SOURCE</b>	Homo sapiens		
<b>ORGANISM</b>	Homo sapiens (human)		
<b>REFERENCE</b>	Makrilia; Eutheria; Primates; Catarrini; Hominidae; Homo. I (bases 1 to 172571)		
<b>AUTHORS</b>	Muzny,D.M., Adams,B., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayle,M., Banks,T., Barberia,J., Benton,J., Bimonte,K., Blankenburg,K., Bonin,D., Bouck,J., Bowie,S., Briava,M., Brown,E., Brown,M., Bryant,N.P., Buhan,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavaos,S.R., Chacko,J.J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davis,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Den,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Barnhart,C., Edgar,D., Edwards,C.C., Elhai,C., Emerling,S., Escott,M., Failes,T., Ferrando,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,J., Hart,M., Havlik,P., Hawes,A., Hernandez,J., Hernandez,O., Hodges,A., Hogenesch,B.,		
<b>Db</b>	386 CCTCTCTCCAGACTACACACCGGCCACTGCGGAGCTGCAAGCATGTAACCTG	<b>Qy</b>	369 GCTTCCTGTTGCAACTGCACCATCTGCAATGTCAGTGAGTGCTGCGTCCAATGCT
<b>Qy</b>	428		
<b>Db</b>	446 GTTTCTTATTCGGCAACTGCACTGCACTGCAATGTCAGTGCACTGCACTGCAAGACT	<b>Db</b>	505
<b>Qy</b>	505		
<b>Db</b>	429 GGGAGTGAGGACAGAGTGACTGGCAGGCCACCTGCGATCCCTCCAAACGCCCTGCTGAGCG	<b>Qy</b>	488
<b>Qy</b>	565		
<b>Db</b>	506 GGGAGTGAGGACAGAGTGACTGGCAGGCCACCTGCGATCCCTCCAAACGCCCTGCTGAGCG	<b>Qy</b>	565
<b>Qy</b>	565		
<b>Db</b>	489 CTGGCTCTCAGGCCACCCACTTACCTTGCTG	<b>Qy</b>	548
<b>Qy</b>	548		
<b>Db</b>	556 GAGACCACTCTGAGGCCACGCCACACCACCACTTACCTTGCTG	<b>Db</b>	625
<b>Qy</b>	625		
<b>Db</b>	549 AGATGCTGAGGCCAGAGTGCGACATCGAGCTCTGCTGACTTCAGGCGACTG	<b>Db</b>	608
<b>Qy</b>	608		
<b>Db</b>	626 AGAGC-----CATCTGSCCCCTACA-----CAGGCGACTTC	<b>Db</b>	658
<b>Qy</b>	658		
<b>Db</b>	609 CTGGCCGAGCTCTCACCCACTGGCAGCCACCCAGATCCCTGTTGAGCTCGATT	<b>Qy</b>	668
<b>Qy</b>	668		
<b>Db</b>	659 CCACTTGACTGACTCTATAGCCAGGGCATCCATGACCTGAGCTGGACTGCA	<b>Db</b>	718
<b>Qy</b>	718		
<b>Db</b>	669 TTGGCATCTTGATCTCTGAGTAGTCTCTGTTTACCCCTGGCGCCCTGT	<b>Qy</b>	728
<b>Qy</b>	728		
<b>Db</b>	719 TCGGATCTTGTGACTCTTCAGCACTGTTCTATCTCTCTCTGGTGAATCTGT	<b>Db</b>	778
<b>Qy</b>	778		
<b>Db</b>	729 TCTCTCCATCAACGAGGAATATAGATCAACAAAGGAAAGTCCCTGCTGCGCTCGAG	<b>Qy</b>	788
<b>Qy</b>	788		
<b>Db</b>	777 TCTTCCATCAACGAGGAACCAACGGGGCA---AATGAGACCGGGAGCGAGCTGCTGAG	<b>Db</b>	835
<b>Qy</b>	835		
<b>Db</b>	789 AGCTTCTGTTAAGCTGGCCAGGGAGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	<b>Qy</b>	848
<b>Qy</b>	848		
<b>Db</b>	836 AGCTTCTGTTAAGCTGGCCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	<b>Db</b>	895
<b>Qy</b>	895		
<b>Db</b>	849 ATTACCGAAACCGGAGCCTGCTGCTGCCCCCTGAGCCAGCACCTGCGGTAGTGCATA	<b>Qy</b>	908
<b>Qy</b>	908		
<b>Db</b>	896 ACTTACCGAAACCGGAGCCTGCTGACCCCTGAGCCAGCACCTGCGGTAGTGCATA	<b>Db</b>	955
<b>Qy</b>	955		
<b>Db</b>	909 CAGCCCTGCTCCACCCACCCC 933	<b>Db</b>	980
<b>Qy</b>	980		
<b>Db</b>	956 AGGGGGCCATTCAGAGAGCTC	<b>Db</b>	980
<b>Qy</b>	980		

Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jain,Y., Johnson,R., Jolani,S., Joudan,B., Karisson,B., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kravovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,L.H., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H., Lozada,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheswari,M., Mapua,P., Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,B., Mawhinney,B., McLeod,M.P., Meador,M., Mez,G., Mercier,S., Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T., Scherer,S., Scott,G., Shen,H., Shim,C., Shoshtari,N., Sisson,I., Sodergren,E., Soniske,T., Sparks,A., Stanley,H., Stodd,H., Sutton,A., Svatek,A., Tabor,P., Tammeria,A., Tammeria,K., Tang,H., Tansey,J., Taylor,T., Rolfe,M., Ruiz,S., Savery,G., Uismani,K., Vasquez,L., Vera,V., Villalon,D., Vinton,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R., Weinstock,G. and Gibbs,R.

**TITLE** Direct Submission  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 172571)  
**AUTHORS** Worley,K.C.

**TITLE** Direct Submission  
**JOURNAL** Submitted (26-Nov-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
**REFERENCE** 3 (bases 1 to 172571)  
**AUTHORS** Worley,K.C.

**TITLE** Direct Submission  
**JOURNAL** Submitted (07-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
**REFERENCE** 4 (bases 1 to 172571)  
**AUTHORS** Worley,K.C.

**TITLE** Direct Submission  
**JOURNAL** Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
**REFERENCE** 5 (bases 1 to 172571)  
**AUTHORS** Worley,K.C.

**TITLE** Direct Submission  
**JOURNAL** Submitted (01-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
**COMMENT** On Feb 1, 2003 this sequence version replaced gi:4575650.  
**INFORMATION** <http://www.hgsc.bcm.tmc.edu/> or email  
**gc-help@bcm.tmc.edu**

**CLONE LENGTH:** This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

**ANNOTATION OF FEATURES:**

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences. Genes and regions of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

**SEQUENCING READ COVERAGE:** Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

**QUALITY OF INDIVIDUAL BASES:** This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

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repeat_region	/mol type="genomic DNA"
repeat_region	/db_xref="taxon:9606"
repeat_region	/chromosome="12"
repeat_region	/clone="RP5-940J5"
repeat_region	8. .226
repeat_region	/rpt_family="Alusg/x"
repeat_region	1434. .1665
repeat_region	/rpt_family="MER46C"
repeat_region	complement(3417. .3568)
repeat_region	/rpt_family="AluJo/FRAM"
repeat_region	/clone="RP5-940J5"
repeat_region	3893. .3916
repeat_region	/rpt_family="(CA)n"
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repeat_region	/rpt_family="Alusg"
repeat_region	complement(4733. .4992)
repeat_region	/rpt_family="LIPAS5"
repeat_region	5615. .5901
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repeat_region	4735. .4759
repeat_region	/rpt_family="LIMB7"
repeat_region	6058. .6083
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repeat_region	complement(6084. .6101)
repeat_region	/rpt_family="LIMB7"
repeat_region	complement(6102. .6412)
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repeat_region	complement(6420. .6551)
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repeat_region	6556. .6668
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repeat_region	6685. .6993
repeat_region	/rpt_family="AluSg"
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STS	8519. .8823
STS	/standard_name="WI-7129"
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repeat_region	/rpt_family="MER97b"
repeat_region	12769. .12877
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ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE I (bases 1 to 10529)  
 AUTHORS Livingston, R.J., Reider, M.J., Chung, M.-W., Ritchie, T.K.,  
 Olson, A.N., Nguyen, C.P., Poel, C.L., Robertson, P.D.,  
 Schackwitz, W.S., Sherwood, J.K., Sherwood, A.M., Leithauer, B.J. and  
 Nickerson, D.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-DEC-2003) Genome Sciences, University of Washington,  
 1705 NE Pacific, Seattle, WA 98195, USA  
 COMMENT To cite this work, please use: NIEHS-SRS, Environmental Genome  
 Project, NIEHS ES1478, Department of Genome Sciences, Seattle, WA  
 (URL: <http://esgp.gs.washington.edu>).  
 FEATURES location/Qualifiers  
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 variation /organism="Homo sapiens"  
 /mol\_type="Genomic DNA"  
 /db\_xref=Taxon:9606  
 variation 127  
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RESULT 12

AY504961 LOCUS AY504961 10529 bp DNA linear PRI 27-DEC-2003 DEFINITION Homo sapiens tumor necrosis factor receptor superfamily, member 7 ACCESSION AY504961 VERSION AY504961.1 GI:40288428 KEYWORDS SOURCE Homo sapiens (human)



AC005840/c AC005840 140026 bp DNA linear PRI 20-OCT-2000  
 LOCUS Homo sapiens complete sequence of a PAC clone RP1-102E24 containing SIB1, CD27, and SCNNA genes.  
 DEFINITION AC005840 AC005840 VERSION AC005840-2 GI:10938025 HTG.

KEYWORDS SOURCE  
 ORGANISM Homo sapiens (human)  
 SOURCE  
 HOME sapiens  
 HOME sapiens (human)

ORGANISM  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS  
 1 Morris, D.W., Morris, D.W. and Malandro, M.S.  
 TITLE Novel therapeutic targets in cancer  
 JOURNAL Patent: WO 2004074320-A4 02-SEP-2004;  
 Sagres Discovery, Inc. (US)  
 FEATURES Location/Qualifiers  
 1. -2815 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Query Match 36.9%; Score 442.8; DB 6; Length 26815;  
 Best Local Similarity 99.6%; Pred. No. 5e-97; 0; Mismatches 2; Indels 0; Gaps 0;  
 Matches 444; Conservative 0; Unaligned 0;

OY 756 CAAACAMGGAGAAGTCCTGTGGAGCCCTGCAGGCCCTGCGTACAGCTGCCAGGG 815  
 Db 16367 CAGACAAGGGAGAACGCTTGCGTGGAGCCCTGCAGGCCCTGCGTACAGCTGCCAGGG 16426  
 OY 816 AGGGAGGGAGCACCATCCCATCCAGGAGATTACCGAAACCGGAGCTGCTGCT 875  
 Db 16427 AGGGAGGGAGCACCATCCCATCCAGGAGATTACCGAAACCGGAGCTGCTGCT 16486  
 OY 876 CCCCTGTGGAGCACCTGGTAGCTGCTGAGCTGCTACAGCCCTGGCTCCACCCCCACCCGG 935  
 Db 16487 CCCCTGTGGAGCACCTGGTAGCTGCTGAGCTGCTACAGCCCTGGCTCCACCCCCACCCGG 16546  
 OY 936 CGACCATCCAGGGAGGTGAGACTGGCGCCAACCTGAGTCCTCCATCTTGTCAG 995  
 Db 16547 CGACCATCCAGGGAGGTGAGACTGGCGCCAACCTGAGTCCTCCATCTTGTCAG 16606  
 OY 996 GGCCCTTCTCTGTGTACAGCTGAGCAGAGTCCTTCTGAGACTGGAGGAGGAGCA 1055  
 Db 16607 GGCCCTTCTCTGTGTACAGCTGAGCAGAGTCCTTCTGAGACTGGAGGAGGAGCA 16666  
 OY 1056 ATATGGAGGAGGTGAGCTGGAGCAGGAGCCAGGCCAGCTGGCTGGCG 1115  
 Db 16667 ATATGGAGTGGTGTGAGCTGGAGCAGGAGCCAGGCCAGCTGGCTGGCG 16726  
 OY 1116 GGCGGGAGCTCTGGTGTGAAACACACTTCTGCGTGGAGAACCCACATGTACAGA 1175  
 Db 16727 GGCGGGAGCTCTGGTGTGAAACACACTTCTGCGTGGAGAACCCACATGTACAGA 16786

AC005840/c AC005840 140026 bp DNA linear PRI 20-OCT-2000  
 LOCUS Homo sapiens complete sequence of a PAC clone RP1-102E24 containing SIB1, CD27, and SCNNA genes.  
 DEFINITION AC005840 AC005840 VERSION AC005840-2 GI:10938025 HTG.

KEYWORDS SOURCE  
 ORGANISM Homo sapiens (human)  
 SOURCE  
 HOME sapiens  
 HOME sapiens (human)

ORGANISM  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS  
 1 (bases 1 to 140026) Montgomery,K.T., Lau,S.T. and Kucherlapati,R.  
 TITLE High Throughput Sequencing of Human Chromosome 12  
 JOURNAL Unpublished  
 REFERENCE AUTHORS  
 2 (bases 1 to 140026) Montgomery,K.T., Lau,S.T. and Kucherlapati,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-OCT-1998) Department of Molecular Biology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10461, USA  
 REFERENCE AUTHORS  
 3 (bases 1 to 140026) Montgomery,K.T., Lau,S.T. and Kucherlapati,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-OCT-2000) Department of Molecular Genetics, Albert Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA  
 COMMENT On Oct 20, 2000 this sequence version replaced gi:3779004.  
 ----- Genome Center:  
 Albert Einstein College of Medicine  
 Code: AECOM  
 Web Site: <http://sequence.aecom.yu.edu/chrl2/>  
 Contact: jhan@sequence.aecom.yu.edu

CLOSE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Features listing.

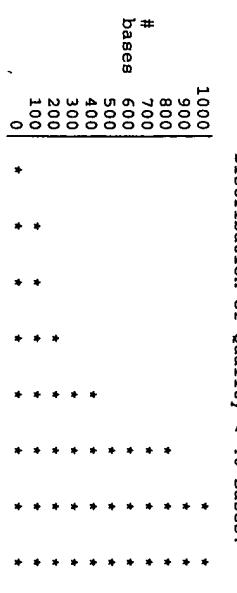
ANNOTATION OF FEATURES:  
 SRSB are identified using ePCR (Genome Res. 7:541-550).  
 Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for human sequences.  
 Genes and Regions of sequence similarity are identified by BLAST (Nuc. Acid Res. 25:3389-3402) similarity (expect < 1e-34) to EST and cDNA Sequences in UniGene. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Attempts are made to complete double stranded sequence for all regions. All sequence is completed to a standard of coverage with a minimum of 3 reads with no ambiguities. If the sequence coverage for a region does not meet this standard, it is indicated in the annotation as Low Coverage. Low Coverage linkages are verified by PCR product size verification or verification of forward and reverse reads from clones which span the low coverage area.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated average error rate is less than 1 per 10,000 bases using the Consed quality parameters. Regions that do not meet this requirement are annotated as Low Quality.

----- Summary Statistics  
 Center Project name: RPI-102E24  
 Sequencing vector: M13  
 Chemistry: Dye-Terminator Big Dye; 100<sup>t</sup>  
 Assembly program: Phrap version 0.990319  
 Contig length: 140026  
 Fraction of Phrap value < 40: 0.0426  
 Error Rate in Consed: 0.56 per 10,000 bases  
 Number of N's in consensus: 1

## ----- Distribution of Quality &lt; 40 Bases:

FEATURES  
Source

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repeat_region complement(11678. .11692)
repeat_region /rpt_family="FFRM"
repeat_region complement(11693. .11995)
repeat_region /rpt_family="AluJb"
repeat_region complement(11956. .12157)
repeat_region /rpt_family="FFRM"
repeat_region 12547. .12899
repeat_region /rpt_family="MER104"
repeat_region complement(12900. .13198)
repeat_region /rpt_family="AluX"
repeat_region 13199. .13254
repeat_region /rpt_family="MER104"
repeat_region complement(13309. .13472)
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repeat_region complement(18210. .18342)
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repeat_region complement(18391. .18519
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repeat_region /rpt_family="TIRIA_int"
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QY 816 AGGAGGGGAGCACATCCCATCAGGGGATTCGAAACGGAGGCTGCGCTGCT 875
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QY 876 CCCCTCTAGCCAGCACTGCGAGCTGCACTACGGCTGACCTGACCCACCGGC 935
Db 33359 CCCCTCTAGCCAGCACTGCGAGCTGCACTACGGCTGACCTGACCCACCGGC 33300
QY 936 CGACCATCCAAGGGAGAGTGGAGACCTGCGACCCACACTGCGATCCATCTGTCAG 995

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RESULT 15

HUMCD27AGB

LOCUS HUMCD27AGB

DEFINITION Human antigen CD27 gene, exons 4-5.

ACCESSION L24494

VERSION L24494.1

PRI 24-SEP-1993

KEYWORDS antigen.

SOURCE Homo Sapiens (human)

ORGANISM Homo Sapiens

REFERENCE 1 (bases 1 to 2365)

AUTHORS Loepen,W.A., Gravesen,L.A., Beumer,S., Melfi,C.J., Hagemeyer,A. and Borst,J.

TITLE Genomic organization and chromosomal localization of the human CD27 gene

JOURNAL J. Immunol. 149 (12), 3937-3943 (1992)

MEDLINE 93094588

PUBMED 1334106

COMMENT Original source text: Homo sapiens peripheral blood DNA.

Chromosome 12p13.

FEATURES Location/Qualifiers

1. .2365 "Homo sapiens"

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/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/tissue\_type="peripheral blood"

/germline

ORIGIN

Query Match Score 408.8; DB 9; Length 2365;

Best Local Similarity 97.0%; Pred. No. 1.e-88;

Matches 436; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

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Db 1824 AGGGAGGGAGGAGCACCATCCCCATCCAGGAGGATTACCGAAACGGAGGCCAGG 1883

QY 876 CCCCTGAGGAGCACCTGGAGCTGCACTACAGCCCTGGCTCCACCCACCCGC 935

Db 1884 CCCCTGAGGAGCACCTGGG- AGCTGCACTACAGCCCTGGCTCCACCCACCCGC 1942

QY 936 CGACCATCGAGGAGGAGCTGGAGCTGGAGCCAACTGCACTCCATCTGTGAG 995

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